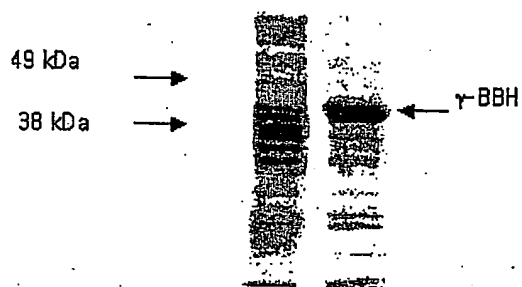


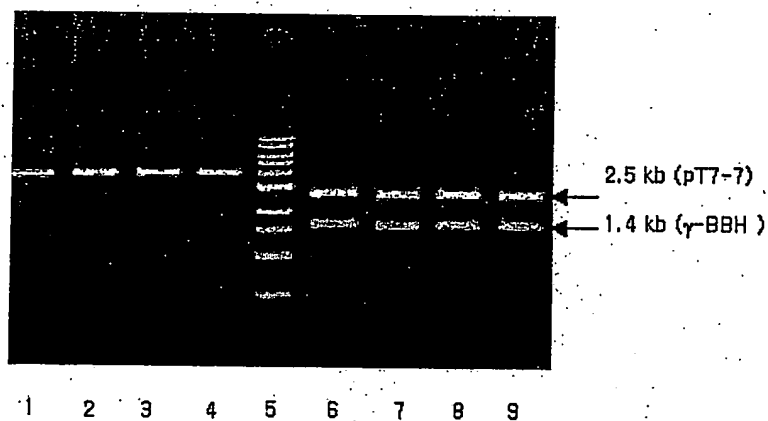
1/3

1



Lane 1 : Protein molecular size marker,
Lane 2 : E.coli BL21 w/o g -BBH gene,
Lane 3 : E.coli BL21 w/ g -BBH gene and Induced by 1mM IPTG

2



Lane 1~4 : pT7-7 + g-BBH plasmid digested with Nde I
Lane 5 : 1kb DNA ladder
Lane 6~9 : pT7-7 + g-BBH plasmid digested with Nde I and Sal I

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2/3

3

CLUSTAL W (1.82) multiple sequence alignment

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Human      -----NACTIQKAEALDGAHLMQILWYDEEESLPAVWLRDNCPCSDCYLDSAKARK 52
rat        -----NHCAILKAEAVDGAHLMQIFWHDGAESLPAVWLRDNCQCSDCYLHSAKARK 52
pseudomonas NA|ADVRTFPLISPLASAAASFASGVSYT@ADGRVSPFHNLWLRDNCPCGDCVVEVTREQV 60
N.crassa   -----NATAAVQVSYPAPVGPDP|GYAPDHDKYLARVKKRRRENEKLESSLPPG 48
          : : : : : * : : : :

Human      LLVEALDYNIGIKGLIFDRK-KVYIT@PDEHVSEFQAD@LKKRCFSQARAKLQRELF 111
rat        LLLEALDYNIRNDOLTFDQK-KVYIT@PNGHVSEFEAN@LKKRCFSQEARAGLQBELFLP 111
pseudomonas FLVADVPEDIQVQAVTIGDDGRLVYQ@DGHASAVHPG@LRAHAYDAQSLA-EREAAAP 118
N.crassa   -FPRRLDSDLVWDGNTLAETVDWTVRLTEEAIDEIEALRHFKSLNKLPGYINQETFLP 107
          : : : : : * : : : :

Human      EDQVW@GSELQLPTLDFEDVLRVDEHAYK@LSTLKKV@IYRLTGAADKPGVSKLQKRMGF 171
rat        EDQVW@GSELQLPTLNFEDVLRNDDHAYK@LSSLLKKV@IYRLTGAADKRGEEI|KLGRIGF 171
pseudomonas HKHPRW@QGLSLPVYDHGAVNQDDDTLLEWLLAVRDVQLTQLHGVPTEPGAL|PLAKRISF 178
N.crassa   RLHHTLRSLSHLHGHGFKYLR-GLPVTSHRENI|IYAGVSSHVAPIRGRQDNQ-H 164
          : : : : : * : : : :

Human      LVLTFYGH@QVQDKIDANNVAVTTGKLSFHTDVPALHHPG-VQLLHC|KQTYTGGDSE 230
rat        LVLTFYGH@QVQDKIDANNVAVTTGKLSFHTDVPALHHPG-VQLLHC|KQTYTGGDSE 230
pseudomonas IRESNFGVLFDRSKADADSNVTAFLPLHLDLPTRELQPG-LQFLHCLYNDATGGNST 237
N.crassa   NGHPPADVYLAHIKDLSTTVSDVSKI|GAPAVTTEKQVFTDAGDI|VALFCLGEAAEGGSY 224
          : : : : : * : : : :

Human      IVDGFNVQCKLKKNNPQAFQILSS-TFVDFTD|GY-----DYCDFSVQSKHKI|ELDDK 283
rat        IVDGFNVQCKLKEKNPQAFSILSS-TFVDFTD|GY-----DYCDFSVQSKHKI|ELDDK 283
pseudomonas FVDGFAIAEALRIEAPAAVRLICE--TPVEFRNK-----DRHSDVRCIAPVIALDSS 287
N.crassa   LSSSVKYVNELAATRPDLVRTLAEPVVADEFGKEGRKFSVRPLLHFQSTAAAASREAKPE 284
          : : : : : * : : : :

Human      GQVYRINFNNAITRDTIFDVP-VERVQPFYAALKEFVDMN-SKESKFTFKNNPGDVITF 340
rat        GQVYRINFNNAITRDTVFDVP-IERVQPFYAALKEFVDMN-SKEYKYTFKNNPGDVITF 340
pseudomonas GEVREIRLANFLR-APFQND-AQRMPDYVLAIRRFIQNTR-EPRFCFTRLEAGLWCF 343
N.crassa   SERLI|QVARRFTGYWGLPRSD|PPI|TEAQAEALDALHFTAECYAVALLDFRGGVQFV 344
          : : : : : * : : : :

Human      DNWRLHGRRSVEAGTEISRHLEGAYAD-----@DVVMS-RLRIL 379
rat        DNWRLHGRRSVEAGTEISRHLEGAYAD-----@DVVMS-RLRIL 379
pseudomonas DNRRVLHARDADFP-ASGDPHFGQCYVD-----ADELLS-RLVL 381
N.crassa   NNLSVFHSRAGFRDEGEKQHLVRL@LRDPENAWETPEALKERWERYVGGVSPEREVPL 404
          : * : : : : * : : : :

Human      RQRVENGN-----387
rat        RQRVMNGN-----387
pseudomonas QR-----383
N.crassa   EPQIRASAKGESYGTQGGGGY 425

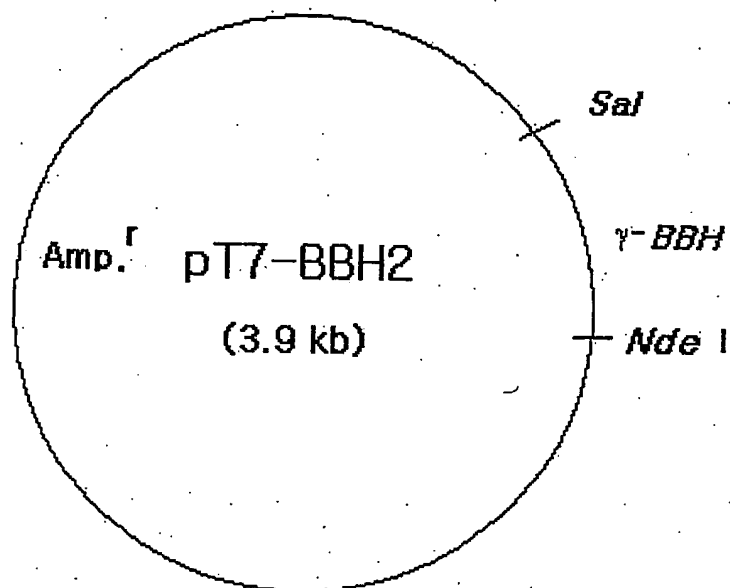
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(Sequences were aligned using the European Bioinformatics Institute (EMBL-EBI) sequence analysis program, clustalW.)

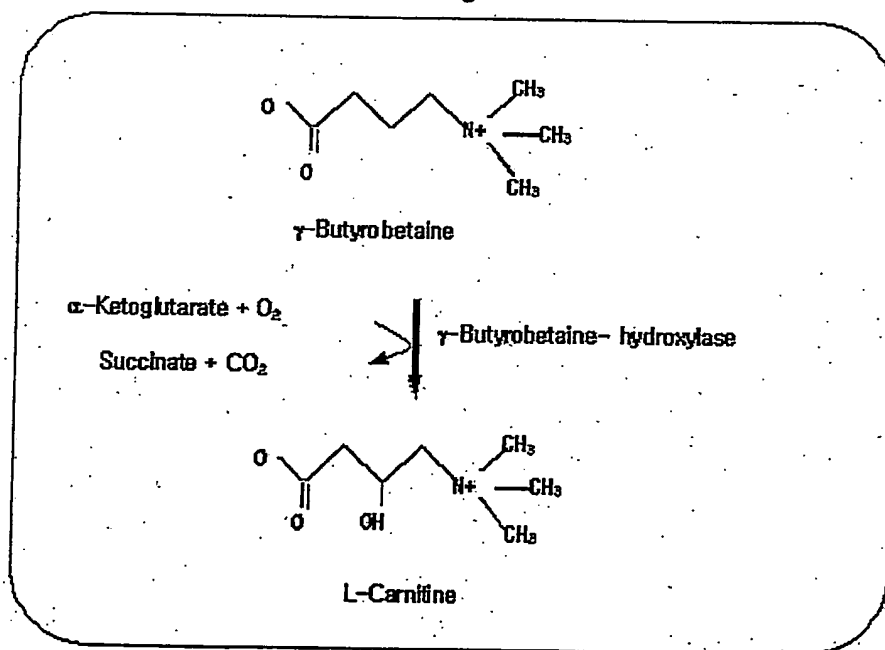
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3/3

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